



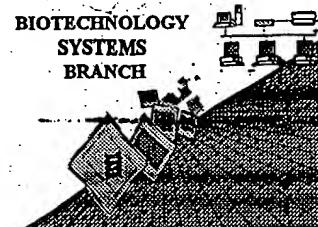
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SEP 30 2002

OFFICE OF PETITIONS

**RAW SEQUENCE LISTING  
ERROR REPORT**



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/636,530

Source: OIP E

Date Processed by STIC: 8/17/2000

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR FURTHER INFORMATION, PLEASE TELEPHONE MARK SPENCER, 703-308-4212.

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 3.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

**Checker Version 3.0**

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:  
<http://www.uspto.gov/web/offices/pac/checker>



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## Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION		SERIAL NUMBER: 09/636536
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE		
1 _____ Wrapped Nucleics	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3, as this will prevent "wrapping".	
2 _____ Wrapped Aminos	The amino acid number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3, as this will prevent "wrapping".	
3 _____ Incorrect Line Length	The rules require that a line not exceed 72 characters in length. This includes spaces.	
4 <input checked="" type="checkbox"/> Misaligned Amino Acid Numbering	The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.	
5 _____ Non-ASCII	This file was not saved in ASCII (DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text so that it can be processed.	
6 _____ Variable Length	Sequence(s) _____ contain n's or Xaa's which represented more than one residue. As per the rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.	
7 _____ PatentIn ver. 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
8 _____ Skipped Sequences (OLD RULES)	Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (i) SEQUENCE CHARACTERISTICS: (Do not insert any headings under "SEQUENCE CHARACTERISTICS") (xi) SEQUENCE DESCRIPTION: SEQ ID NO:X: This sequence is intentionally skipped  Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).	
9 _____ Skipped Sequences (NEW RULES)	Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence. <210> sequence id number <400> sequence id number 000	
10 _____ Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Use of <220> to <223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.	
11 _____ Use of <213> Organism (NEW RULES)	Sequence(s) _____ are missing this mandatory field or its response.	
12 _____ Use of <220> Feature (NEW RULES)	Sequence(s) _____ are missing the <220> Feature and associated headings. Use of <220> to <223> is MANDATORY if <213> ORGANISM is "Artificial" or "Unknown". Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new	
13 _____ PatentIn ver. 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other means to copy file to floppy disk.	



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OIPE

RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/636,530  
DATE: 08/17/2000  
TIME: 10:08:21  
Input Set : A:\CIP pharma Sequence Listing Ascii.txt  
Output Set: N:\CRF3\08162000\I636530.raw

Does Not Comply  
Corrected Diskette Need

OK  
WOK  
4 <110> APPLICANT: Cantor, Thomas L.  
6 <120> TITLE OF INVENTION: Parathyroid Hormone Antagonists or Modulators and Uses Therefor  
9 <140> CURRENT APPLICATION NUMBER: US/09/636,530  
9 <141> CURRENT FILING DATE: 2000-08-10  
0 <130> FILE REFERENCE:  
9 <160> NUMBER OF SEQ ID NOS: 5  
11 <170> SOFTWARE: Microsoft Word 2000 - ASCII format

*Suggestion: Cons  
new sequence*

ERRORED SEQUENCES

14 <210> SEQ ID NO: 1  
16 <211> LENGTH: 84 ~~{integer length}~~  
18 <212> TYPE: PRT  
20 <213> ORGANISM: human parathyroid hormone peptide fragment  
22 <400> SEQUENCE: 1  
24 Ser Val Ser Glu Ile Gln Leu Met His Asn Leu Gly Lys His Leu  
25 1 5 10 15  
27 Asn Ser Met Glu Arg Val Glu Trp Leu Arg Lys Lys Leu Gln Asp  
28 20 25 30  
30 Val His Asn Phe Val Ala Leu Gly Ala Pro Leu Ala Pro Arg Asp  
31 35 40 45  
33 Ala Gly Ser Gln Arg Pro Arg Lys Lys Glu Asp Asn Val Leu Val  
34 50 55 60  
36 Glu Ser His Glu Lys Ser Leu Gly Glu Ala Asn Lys Ala Asp Val  
37 65 70 75  
E--> 39 Asn Val Leu Thyr Lys Ala Lys Ser Gln 80  
40  
43 <210> SEQ ID NO: 2  
45 <211> LENGTH: 83 ~~{integer length}~~  
47 <212> TYPE: PRT  
49 <213> ORGANISM: human parathyroid hormone peptide fragment  
51 <400> SEQUENCE: 2  
53 Val Ser Glu Ile Gln Leu Met His Asn Leu Gly Lys His Leu Asn  
54 1 5 10 15  
56 Ser Met Glu Arg Val Glu Trp Leu Arg Lys Lys Leu Gln Asp Val  
57 20 25 30  
60 His Asn Phe Val Ala Leu Gly Ala Pro Leu Ala Pro Arg Asp Ala  
61 35 40 45  
63 Gly Ser Gln Arg Pro Arg Lys Lys Glu Asp Asn Val Leu Val Glu  
64 50 55 60  
66 Ser His Glu Lys Ser Leu Gly Glu Ala Asn Lys Ala Asp Val Asn  
67 65 70 75  
E--> 69 Val Leu Thyr Lys Ala Lys Ser Gln 80  
70  
73 <210> SEQ ID NO: 3  
75 <211> LENGTH: 51 ~~{integer length}~~

*delete globally do not show template*

*invalid - do not show modifications  
in the sequence itself.*

*Explain in 2207-2212  
section*

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RAW SEQUENCE LISTING      DATE: 08/17/2000  
 PATENT APPLICATION: US/09/636,530      TIME: 10:08:21  
 Input Set : A:\CIP pharma Sequence Listing Ascii.txt  
 Output Set: N:\CRF3\08162000\I636530.raw

```

77 <212> TYPE: PRT
79 <213> ORGANISM: human parathyroid hormone peptide fragment
81 <400> SEQUENCE: 3
83 Phe Val Ala Leu Gly Ala Pro Leu Ala Pro Arg Asp Ala Gly Ser
E--> 84 1 5 10 15
86 Gln Arg Pro Arg Lys Lys Glu Asp Asn Val Leu Val Glu Ser His
E--> 87 20 25 30
89 Glu Lys Ser Leu Gly Glu Ala Asn Lys Ala Asp Val Asn Val Leu
E--> 90 35 40 45
92 Thyr Lys Ala Lys Ser Gln
E--> 93 50
96 <210> SEQ ID NO: 4
98 <211> LENGTH: 82 (integer length)
100 <212> TYPE: PRT
102 <213> ORGANISM: human parathyroid hormone peptide fragment
104 <400> SEQUENCE: 4
106 Ser Glu Ile Gln Leu Met His Asn Leu Gly Lys His Leu Asn Ser
107 1 5 10 15
109 Met Glu Arg Val Glu Trp Leu Arg Lys Lys Leu Gln Asp Val His
110 20 25 30
112 Asn Phe Val Ala Leu Gly Ala Pro Leu Ala Pro Arg Asp Ala Gly
113 35 40 45
115 Ser Gln Arg Pro Arg Lys Lys Glu Asp Asn Val Leu Val Glu Ser
116 50 55 60
118 His Glu Lys Ser Leu Gly Glu Ala Asn Lys Ala Asp Val Asn Val
119 65 70 75
E--> 121 Leu Thyr Lys Ala Lys Ser Gln
122 80
126 <210> SEQ ID NO: 5
128 <211> LENGTH: 57 (integer length)
130 <212> TYPE: PRT
132 <213> ORGANISM: human parathyroid hormone peptide fragment
134 <400> SEQUENCE: 5
136 Leu Gln Asp Val His Asn Phe Val Ala Leu Gly Ala Pro Leu Ala
137 1 5 10 15
139 Pro Arg Asp Ala Gly Ser Gln Arg Pro Arg Lys Lys Glu Asp Asn
140 20 25 30
142 Val Leu Val Glu Ser His Glu Lys Ser Leu Gly Glu Ala Asn Lys
143 35 40 45
E--> 145 Ala Asp Val Asn Val Leu Thyr Lys Ala Lys Ser Gln
146 50 55
  
```

*involved*

*misaligned amino acids -  
 see item 4 on Error  
 summary sheet*

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VERIFICATION SUMMARY                      DATE: 08/17/2000  
PATENT APPLICATION: US/09/636,530              TIME: 10:08:22

Input Set : A:\CIP pharma Sequence Listing Ascii.txt  
Output Set: N:\CRF3\08162000\I636530.raw

L:9 M:270 C: Current Application Number differs, Replaced Current Application No  
L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:0 M:201 W: Mandatory field data missing, FILE REFERENCE  
L:39 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
L:39 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1  
L:69 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
L:69 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1  
L:84 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:3  
M:332 Repeated in SeqNo=3  
L:92 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
L:92 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1  
L:121 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
L:121 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1  
L:145 M:333 E: Wrong sequence grouping, Amino acids not in groups!  
L:145 M:320 E: (1) Wrong Nucleic Acid Designator, NUMBER OF INVALID KEYS:1